SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: FALB, DEAN A.

  (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
       TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

 (iii) NUMBER OF SEQUENCES: 38

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   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
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     (B) FILING DATE: 07-JUN-1995
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(viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 288 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: both
     (D) TOPOLOGY: unknown

  (ii) MOLECULE TYPE: cDNA

 (iii) HYPOTHETICAL: NO

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTTAGATG CAGCCTGCAA ATTAAACTTT GATTTTTCAT CTTGTGAAAG CAGTCCTTGT   60

TCCTATGGCC TAATGAACAA CTTCCAGGTA ATGAGTATGG TGTCAGGATT TACACCACTA   120

```
ATTTCTGCAG GTATATTTTC AGCCACTCTT TCTTCAGCAT TAGCATCCCT AGTGAGTGCT      180

CCCAAAATAT TTCAGGCTCT ATGTAAGGAC AACATCTACC CAGCTTTCCA GATGTTTGCT      240

AAAGGTTATG GGAAAAATAA TGAACCTCTT CGTGGCTGCA TCTAAGCC                  288
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 178 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
AAAAATAAAT AAATTAAAGT CTGAGACCAA TTTGCCACTG TGAATATAAG CACATTAACC       60

CCAGGAGGAG CCAAGAACTA CACAAACCTC TCTATGAGAA TTTACCAGTC TTCTTTCATT      120

TGGCAAGAAA AAGCTCAGGA AAATTTGCTT GTTTAAATTC TATGAGCCTA GTCTATGG       178
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 101 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GGGTAATTCA TTAATTACAC TTTAAAATTG GAAAGTGGGA TAAGAAATCT AAAGTAAACC       60

AGCTTATCTT TGAAACAATA TTATTTTGAA ATTGGCTTTA A                         101
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 184 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GGCTTGGTGG TGATGCCTAC AAGAAATGTT TACATACAAA CACTCTATAC ATCTAACTCC        60

CGAAAAAGGA CCAGCTATTT CGGCAACAGA AAAAAGACAA GCATTTCAGA GGAGCGTTGC       120

TTTCCTTAAA GACCTAACTC ACTTAAGTCT TACAAACAGA AATAACAAGG AGGACAATTT       180

TCTA                                                                   184
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 284 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CTTGGGGATG CTGTTTGGAG GAATCCTCAT GAAGCGCTTT GTTTTCTCTC TACAAGCCAT        60

TCCCCGCATA GCTACCACCA TCATCACCAT CTCCATGATC CTTTGTGTTC CTTTGTTCTT       120

CATGGGATGC TCCACCCCAA CTGTGGCCGA AGTCTACCCC CCTAGCACAT CAAGTTCTAT       180

ACATCCGCAG TCTCCTGCCT GCCGCAGGGA CTGCTCGTGC CCAGATTCTA TCTTCCACCC       240

GGTCTGTGGA GACAATGGAA TCGAGTACCT CTCCCCTTGC CATG                       284
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2582 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GGCTTACCAT CGATGCGGCC GCGGATCCAG GGCTCAGAGG GAGGACGCAC CCGCCAGCCA        60

GCCGGGAACC TTCCCTCGCG GGCTCCCAGG GCGGGTCTCT TCCTCTCTCT AGCCCTGCTC       120

AGGCATTCGG CAGGTCCAGC AGAGGTACAC CTCCTGCAGC GGGTTCCAAG TGCACCTCCA       180

GCCTGATGGA CCTGACCAAG GAGGCTTCCA GGAGCACAGA AGGGGCTGCA ACCCAGGTAC       240

CCAGAGAGTG AGCAGCTCCA CGCGGGACTG TGCACGGTGG CCGACACCCG CAGGGACGCC       300

CACCGGACGA GCACGCGGAG GGCCCTCGCC TCCACGGATG CACCATGCCG GTGTGAGGAG       360

CATCTGTTCT TCCCACTCTC TGCAGTTAAC AAACCCAACC CAAACCACCA CAGGTGCTCC       420

TCCTGGGGAG TTTCCTGTCT GACAAATGCC AGGCTCACTT CAAGGAGAAT CACGCTTCTT       480
```

```
TCTAAAGATG GATTCACCAT TTAAAACAGA GCTCTGGGAG CCTTTCGGCA AATCTTGAAA    540

GCTGCACGGC GCAGAGACAT GGATGTGACT TCCCAAGCCC GGGGCGTAGG CCTGGAGATG    600

TACCCAGGCA CCGCGCAGCC TGCGGCCCCC AACACCACCT CCCCCGAGCT CAACCTGTCC    660

CACCCGCTCC TGGGCACCGG CCTGGCCAAT GGGACAGGTG AGCTCTCGGA GCACCAGCAA    720

TACGTGATCG GCCTGTTCCT CTCGTGCCTC TACACCATCT TCCTCTTCCC CATCGGCTTT    780

GTGGGCAACA TCCTGATCCT GGTGGTGAAC ATCAGCTTCC GCGAGAAGAT GACCATCCCC    840

GACCTGTACT TCATCAACCT GGCGGTGGCG GACCTCATCC TGGTGGCCGA CTCCCTCATT    900

GAGGTGTTCA ACCTGCACGA GCGGTACTAC GACATCGCCG TCCTGTGCAC CTTCATGTCG    960

CTCTTCCTGC GGGTCAACAT GTACAGCAGC GTCTTCTTCC TCACCTGGAT GAGCTTCGAC   1020

CGCTACATCG CCCTGGCCAG GGCCATGCGC TGCAGCCTGT TCCGCACCAA GCACCACGCC   1080

CGGCTGAGCT GTGGCCTCAT CTGGATGGCA TCCGTGTCAG CCACGCTGGT GCCCTTCACC   1140

GCCGTGCACC TGCAGCACAC CGACGAGGCC TGCTTCTGTT TCGCGGATGT CCGGGAGGTG   1200

CAGTGGCTCG AGGTCACGCT GGGCTTCATC GTGCCCTTCG CCATCATCGG CCTGTGCTAC   1260

TCCCTCATTG TCCGGGTGCT GGTCAGGGCG CACCGGCACC GTGGGCTGCG GCCCCGGCGG   1320

CAGAAGGCGC TCCGCATGAT CCTCGCAGTG GTGCTGGTCT TCTTCGTCTG CTGGCTGCCG   1380

GAGAACGTCT TCATCAGCGT GCACCTCCTG CAGCGGACGC AGCCTGGGGC CGCTCCTTGC   1440

AAGCAGTCTT TCCGCCATGC CCACCCCCTC ACGGGCCACA TTGTCAACCT CGCCGCCTTC   1500

TCCAACAGCT GCCTAAACCC CCTCATCTAC AGCTTTCTGG GGAGACCTT CAGGGACAAG   1560

CTGAGGCTGT ACATTGAGCA GAAAACAAAT TTGCCGGCCC TGGACCGCTT CTGTCACGCT   1620

GCCCTGAAGG CCGTCATTCC AGACAGCACC GAGCAGTCGG ATGTGAGGTT CAGCAGTGCC   1680

GTGTAGACAG CCTTGGCCGC ATAGGCCCAG CCAGGGTGTG ACTCGGGAGC TGCACACACC   1740

TGGGTGGACA CAAGGCACGG CCACGTCATG TCTCTAAACT GCGGTCAGAT GTGGCTTCTG   1800

GCTCCTCGGG CCTCGCGAGG GTCACGCTTG CCTGGTCACC CTGGGGCTGC TTAGGGAAACC   1860

TCAGGACTGG TCACCTTGCA CTCCTCACAC AGAATTGCTA CAATCCCAAA GCGCTCGCCC   1920

CGCAGGGTCC AAAGGCCAGC GGTGACCAGC CTGTCACCCA GCTCCTCCCC GCCAACCCTG   1980

CCTGCCGCTG CACCTGCCCG CTGCTGCAGG AAACATTTCT GACACCGTCG ACCAGGAAAG   2040

CCACACGGAG AGGCCACTGT GGGTGAAGCG CCTCAGTTAC ACAGGAACCC TAAAGCAAAT   2100

CTGCCACCGT GGGGGAACTG ACGCTGGAGA TGCAAGGTGC TGGTGGGTCT GAGCTGGACG   2160

TCGCGGTGTG TCCTCTGTGC CCACGGTCTG AGCTAGCTAG CGCACCGCCG AGTTAAAGAG   2220

GAGAAGGAAA ACATGCTGCT CTGGTGCACG CCTGAGCGTC CTCCATCTTC CAGGATGGCA   2280

GCAATGGCGC TGTGCGGCCT CACCAGGCCC ACGAGGAGCA GCAGCGCTCG GCCCGGAGCA   2340

GCAGGAAGGC CCCTCTGTGG AGCGCCCGCC GTCTGCTCCG GGGTGGTTCA GTCACTGCTT   2400

GTTGACATCA ACATGGCAAT TGCACTCATG TGGACTGGGA CCGTGCGAGC TGCCGTGTGG   2460

GTTAGTCGGG TGCCAGGACA ATGAAATACT CCAGCACCTG TGGCTGACGA ATTCGTTTCT   2520
```

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ACAGAAGTAA CAGCTGGGGA CAACTGCGAT GATGATGTAA AAACCTTCCC ATAAAATAAG   2580

CC   2582

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAGGTGGG CTCCTGCTCA TCCTAGGCAT CGCACTGATT GTTACCTGTT GCAGAAAGAA   60

TAAAAATGAC ATAAGCAAAC TCATCTTCAA AAGTGGAGAT TTCCAAATGT CCCCGTATGC   120

TGAATACC   128

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 12

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTTTTTTTTT TNG   13

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCATGGCTC   10

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: NO

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CACCCCTGGC ATCTTCTCCT TCC   23

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: NO

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCCTCCCCC AGTTCACCCC ATCC   24

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

  (iii) HYPOTHETICAL: NO

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTGATAGAT GGGCACTGTG T   21

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAACACGGCA TTGTCACTAA CT   22

(2) INFORMATION FOR SEQ ID NO:14:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 22 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: NO

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGTCGCGCC CGCCCCTGAA AT   22

(2) INFORMATION FOR SEQ ID NO:15:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: NO

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCCCTGGC CACCGTCCGT CTGA   24

(2) INFORMATION FOR SEQ ID NO:16:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 17 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

      (iii) HYPOTHETICAL: NO

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCCTGAAGT ACCCCAT   17

(2) INFORMATION FOR SEQ ID NO:17:

```
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 17 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TAGAAGCATT TGCGGTG                                                    17

(2) INFORMATION FOR SEQ ID NO:18:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 10 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGATGCAGCC                                                           10

(2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 13 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO


    (ix) FEATURE:
         (A) NAME/KEY: misc_feature
         (B) LOCATION: 12


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTTTTTTTT TNA                                                       13

(2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 10 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)
```

(iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCTCCCTCAG   10

(2) INFORMATION FOR SEQ ID NO:21:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 13 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

     (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 12

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTTTTTT TNC   13

(2) INFORMATION FOR SEQ ID NO:22:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGAGAGCAG   10

(2) INFORMATION FOR SEQ ID NO:23:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATTTATAAAG GGGTAATTCA TTA   23

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAAAGCCAA TTTCAAAATA AT   22

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTGGTGATG   10

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGTGCGGGAA   10

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACATGCCGTG   10

(2) INFORMATION FOR SEQ ID NO:28:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 18 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGCCGTGTG GGTTAGTC   18

(2) INFORMATION FOR SEQ ID NO:29:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 22 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATTTTATGGG AAGGTTTTTA CA   22

(2) INFORMATION FOR SEQ ID NO:30:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 10 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AATGCGGGAG   10

(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 12..13

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT TNN   13

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT TCC   13

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGACATGCC   10

(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

```
     (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO



     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CATGCCTGTA GAAAAAGGTT                                              20

(2) INFORMATION FOR SEQ ID NO:35:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO



     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTTCATAGAA TCTAAGCCTA                                              20

(2) INFORMATION FOR SEQ ID NO:36:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 3083 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: both
          (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: cDNA


    (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 16

    (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 30

    (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION: 2911


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCA CGAGGMCAGG AGCTCCTTTW CTGCGTCTCC CATCATGGGG CTTAGGGTTG    60

AGTCTTCAGG TTCTGGGGGC AGGAAGGACG GGCACTCAGG AGGCCCCCTC CCCATCCACA   120

GCCCCTCTTT GGGAGGGGGG AAACTTGGCA ACCCGGGAGG CATGTGGATC TTTTCCTAAG   180

CAAGATGCTG AGCTGGAAAG ATGGGGGTGT AAGGTAATGT CCCAAACTGA AACTTTGCCA   240

GGCACTGGGA GAGGCTGTGA ACTCTTTTCT GGCTTTAGAA TTTAGGTCTA GATCCCAAAA   300

GGCTAAGTAC CCCCTGGGGG CTAACCCAGAG GCATGCCTGG GCTGAGCTGA ACCTTCTGGT   360
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GCACTGGCCC CTGGCTGACT GCTCTTCTGC AGGAAGTTGG AGGAGATTCC TGAAGTTGAT    420

TCCTCAGGCT GGATGTCCAA GGGGGTTGGA GTTTCTGATG TCTTTCTGTC TCCCTCTCTT    480

TTCTTTCTCT CCCTACCAGG TCCACTTCTT TCAGAGGGGC CTGCGGTGCT CTAAAAGTTC    540

TCCTGTTAAA GTTTAGAGCA AATTGGTTAT TATTTTAAAA TCAATAAAAC TTTTAAAAGT    600

ACTAAGACAA CTTCTAAGAG GGGAGTGGAC AGAGGGCCTG GTGGCAGCTC ACAGTTTCTT    660

TTCTGACCTT TGGTCTCACC CACCAAGTGT CCCACCTGAG TGCCCACCTT GCCCACCTGA    720

GGTAATGCCC TGGGGCTCCA CCAGTCCAGA TCCACAGGGC GCAGCCATGT GGGAGTGGCG    780

GCTGATTGTT ACCCAGTAGT GTTGATAGCA CATTATTCAT AACAGCCAAA GAGAGGAAGC    840

AACCCAAATG TCCATTAGCT GATAAATGGA TAAATGAAAT ATGGTACGTC CGAAGAATGG    900

AATATCATTC ACCCATGAAA AAGAACGAAG TCCAGCACCA AAACGTGCTA CAACATGGAT    960

GAACTTCGAT GACTTTGTGC CACATGAAAG AAGAAGCCAG CCACAAAAGG CCATATATTG   1020

TATGAAATGA AATGTCCAGA ATGGGCAAAC CCATAGAGAC ACAAAAATCT CCGCCACCTC   1080

CCTACTCTCG GCTGTCTCCT CGCGACGAGT ACAAGCCACT GGATCTGTCC GATTCCACAT   1140

TGTCTTACAC TGAAACGGAG GCTACCAACT CCCTCATCAC TGCTCCGGGT GAATTCTCAG   1200

ACGCCAGCAT GTCTCCGGAC GCCACCAAGC CGAGCCACTG GTGCAGCGTG GCGTACTGGG   1260

AGCACCGGAC GCGCGTGGGC CGCCTCTATG CGGTGTACGA CCAGGCCGTC AGCATCTTCT   1320

ACGACCTACC TCAGGGCAGC GGCTTCTGCC TGGGCCAGCT CAACCTGGAG CAGCGCAGCG   1380

AGTCGGTGCG GCGAACGCGC AGCAAGATCG GCTTCGGCAT CCTGCTCAGC AAGGAGCCCG   1440

ACGGCGTGTG GGCCTACAAC CGCGGCGAGC ACCCCATCTT CGTCAACTCC CCGACGGCTGG   1500

ACGCGCCCGG CGGCCGCGCC CTGGTCGTGC GCAAGGTGCC CCCCGGCTAC TCCATCAAGG   1560

TGTTCGACTT CGAGCGCTCG GGCCTGCAGC ACGCGCCCGA GCCCGACGCC GCCGACGGCC   1620

CCTACGACCC CAACAGCGTC CGCATCAGCT TCGCCAAGGG CTGGGGGCCC TGCTACTCCC   1680

GGCAGTTCAT CACCTCCTGC CCCTGCTGGC TGGAGATCCT CCTCAACAAC CCCAGATAGT   1740

GGCGGCCCCG GCGGGAGGGG CGGGTGGGAG GCCGCGGCCA CCGCCACCTG CCGGCCTCGA   1800

GAGGGGCCGA TGCCCAGAGA CACAGCCCCC ACGGACAAAA CCCCCCAGAT ATCATCTACC   1860

TAGATTTAAT ATAAAGTTTT ATATATTATA TGGAAATATA TATTATACTT GTAATTATGG   1920

AGTCATTTTT ACAATGTAAT TATTTATGTA TGGTGCAATG TGTGTATATG GACAAAACAA   1980

GAAAGACGCA CTTTGGCTTA TAATTCTTTC AATACAGATA TATTTTCTTT CTCTTCCTCC   2040

TTCCTCTTCC TTACTTTTTA TATATATATA TAAAGAAAAT GATACAGCAG AGCTAGGTGG   2100

AAAAGCCTGG GTTTGGTGTA TGGTTTTTGA GATATTAATG CCCAGACAAA AAGCTAATAC   2160

CAGTCACTCG ATAATAAAGT ATTCGCATTA TAGTTTTTTT TAAACTGTCT TCTTTTTACA   2220

AAGAGGGGCA GGTAGGGCTT CAGCGGATTT CTGACCCATC ATGTACCTTG AAACTTGACC   2280

TCAGTTTTCA AGTTTTACTT TTATTGGATA AAGACAGAAC AAATTGAAAA GGGGAGGAAAG   2340

TCACATTTAC TCTTAAGTAA ACCAGAGAAA GTTCTGTTGT TCCTTCCTGC CCATGGCTAT   2400
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GGGGTGTCCA GTGGATAGGG ATGGCGGTGG GGAAAAGGAG AATACACTGG CCATTTATCC    2460

TGGACAAGCT CTTCCAGTCT GATGGAGGAG GTTCATGCCC TAGCCTAGAA AGGCCCAGGT    2520

CCATGACCCC CATCTTTGAG TTATGAGCAA GCTAAAAGAA GACACTATTT CTCACCATTT    2580

TGTGGAAATG GCCTGGGGAA CAAAGACTGA AATGGGCCTT GAGCCCACCT GCTACCTTGC    2640

AGAGAACCAT CTCGAGCCCC GTAGATCTTT TTAGGACCTC CACAGGCTAT TTCCCACCCC    2700

CCAGCCAAAA ATAGCTCAGA ATCTGCCCAT CCAGGGCTGT ATTAATGATT TATGTAAAGG    2760

CAGATGGTTT ATTTCTACTT TGTAAAAGGG AAAAGTTGAG GTTCTGGAAG GATAAATGAT    2820

TTGCTCATGA GACAAAATCA AGGTTAGAAG TTACATGGAA TTGTAGGACC AGAGCCATAT    2880

CATTAGATCA GCTTTCTGAA GAATATTCTC MAAAAAAGAA AGTCTCCTTG GCCAGATAAC    2940

TAAGAGGAAT GTTTCATTGT ATATCTTTTT TCTTGGAGAT TTATATTAAC ATATTAAGTG    3000

CTCTGAGAAG TCCTGTGTAT TATCTCTTGC TGCATAATAA ATTATCCCCA AACTTAAAAA    3060

AAAAAAAAAA AAAAAAACTC GAG                                           3083
```

(2) INFORMATION FOR SEQ ID NO:37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 235 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Met Ser Arg Met Gly Lys Pro Ile Glu Thr Gln Lys Ser Pro Pro Pro
1               5                   10                  15

Pro Tyr Ser Arg Leu Ser Pro Arg Asp Glu Tyr Lys Pro Leu Asp Leu
            20                  25                  30

Ser Asp Ser Thr Leu Ser Tyr Thr Glu Thr Glu Ala Thr Asn Ser Leu
        35                  40                  45

Ile Thr Ala Pro Gly Glu Phe Ser Asp Ala Ser Met Ser Pro Asp Ala
    50                  55                  60

Thr Lys Pro Ser His Trp Cys Ser Val Ala Tyr Trp Glu His Arg Thr
65                  70                  75                  80

Arg Val Gly Arg Leu Tyr Ala Val Tyr Asp Gln Ala Val Ser Ile Phe
                85                  90                  95

Tyr Asp Leu Pro Gln Gly Ser Gly Phe Cys Leu Gly Gln Leu Asn Leu
            100                 105                 110

Glu Gln Arg Ser Glu Ser Val Arg Arg Thr Arg Ser Lys Ile Gly Phe
        115                 120                 125

Gly Ile Leu Leu Ser Lys Glu Pro Asp Gly Val Trp Ala Tyr Asn Arg
    130                 135                 140

Gly Glu His Pro Ile Phe Val Asn Ser Pro Thr Leu Asp Ala Pro Gly
```

```
      145                   150                   155                   160
Gly Arg Ala Leu Val Val Arg Lys Val Pro Pro Gly Tyr Ser Ile Lys
                  165                   170                   175
Val Phe Asp Phe Glu Arg Ser Gly Leu Gln His Ala Pro Glu Pro Asp
              180                   185                   190
Ala Ala Asp Gly Pro Tyr Asp Pro Asn Ser Val Arg Ile Ser Phe Ala
          195                   200                   205
Lys Gly Trp Gly Pro Cys Tyr Ser Arg Gln Phe Ile Thr Ser Cys Pro
      210                   215                   220
Cys Trp Leu Glu Ile Leu Leu Asn Asn Pro Arg
225                   230                   235
```

(2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 375 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Met Asp Val Thr Ser Gln Ala Arg Gly Val Gly Leu Glu Met Tyr Pro
1                   5                   10                   15
Gly Thr Ala Gln Pro Ala Ala Pro Asn Thr Thr Ser Pro Glu Leu Asn
              20                   25                   30
Leu Ser His Pro Leu Leu Gly Thr Ala Leu Ala Asn Gly Thr Gly Glu
          35                   40                   45
Leu Ser Glu His Gln Gln Tyr Val Ile Gly Leu Phe Leu Ser Cys Leu
      50                   55                   60
Tyr Thr Ile Phe Leu Phe Pro Ile Gly Phe Val Gly Asn Ile Leu Ile
65                   70                   75                   80
Leu Val Val Asn Ile Ser Phe Arg Glu Lys Met Thr Ile Pro Asp Leu
              85                   90                   95
Tyr Phe Ile Asn Leu Ala Val Ala Asp Leu Ile Leu Val Ala Asp Ser
          100                   105                   110
Leu Ile Glu Val Phe Asn Leu His Glu Arg Tyr Tyr Asp Ile Ala Val
          115                   120                   125
Leu Cys Thr Phe Met Ser Leu Phe Leu Arg Val Asn Met Tyr Ser Ser
      130                   135                   140
Val Phe Phe Leu Thr Trp Met Ser Phe Asp Arg Tyr Ile Ala Leu Ala
145                   150                   155                   160
Arg Ala Met Arg Cys Ser Leu Phe Arg Thr Lys His His Ala Arg Leu
              165                   170                   175
Ser Cys Gly Leu Ile Trp Met Ala Ser Val Ser Ala Thr Leu Val Pro
              180                   185                   190
```

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```
Phe Thr Ala Val His Leu Gln His Thr Asp Glu Ala Cys Phe Cys Phe
        195                     200                 205

Ala Asp Val Arg Glu Val Gln Trp Leu Glu Val Thr Leu Gly Phe Ile
    210                 215                 220

Val Pro Phe Ala Ile Ile Gly Leu Cys Tyr Ser Leu Ile Val Arg Val
225                 230                 235                 240

Leu Val Arg Ala His Arg His Arg Gly Leu Arg Pro Arg Arg Gln Lys
            245                 250                 255

Ala Leu Arg Met Ile Leu Ala Val Leu Val Phe Phe Val Cys Trp
        260                 265                 270

Leu Pro Glu Asn Val Phe Ile Ser Val His Leu Leu Gln Arg Thr Gln
    275                 280                 285

Pro Gly Ala Ala Pro Cys Lys Gln Ser Phe Arg His Ala His Pro Leu
    290                 295                 300

Thr Gly His Ile Val Asn Leu Ala Ala Phe Ser Asn Ser Cys Leu Asn
305                 310                 315                 320

Pro Leu Ile Tyr Ser Phe Leu Gly Glu Thr Phe Arg Asp Lys Leu Arg
            325                 330                 335

Leu Tyr Ile Glu Gln Lys Thr Asn Leu Pro Ala Leu Asp Arg Phe Cys
        340                 345                 350

His Ala Ala Leu Lys Ala Val Ile Pro Asp Ser Thr Glu Gln Ser Asp
    355                 360                 365

Val Arg Phe Ser Ser Ala Val
    370                 375
```